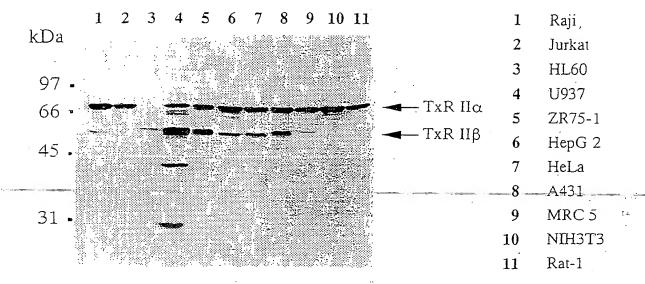


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Figure 1

1'	VGGGGGGTACKTINGGANGGNDIDDDAAGGGGTACTATTATT
. 1"	********** ***** *. MNGPEDLPKSYDYDLIIIGGGSGGLAAKEAAQYGK
	FAD-binding region (ADP.)
61'	KVAVVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWBVAQPVPH
37"	KVMVLDFVTPTPLGTRWGLGGTCVNVGCIPKKLMHQAALLGQALQDSRNYGWKVEETVKH
	Reduction active center
121'	DWRKMAEAVQNHVKSLNWGHRVQLQDRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH
97"	DWDRMIEAVQNHIGSLNWGYRVALREKKVVYENAYGQFIGPHRIKATNNKGKEKIYSAES
181'	IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD
157"	FLIATGERPRYLG-IPGDKEYCISSDDLFSLPYCPGKTLVVGASYVALECAGFLAGIGLG
241'	NADPH-binding domain TTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDST -*-*** *******************************
216"	VTVMVRSILLRGFDQDMANKIGEHMEEHGIKFIRQFVPIKVEQIKAGTPGRLRVVAQSTN
298'	TGKEDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTQKILVDSREATSVPHIYAIGDV ** *** * *** * *******************
276"	SEEIIEGEYNTVMLAIGRDACTRKIGLETVGVKINEKTGKIPVTDEEQTNVPYIYAIGDI FAD-binding region (Flavir
358'	VEGRPELTPTAIMAGRLLVQRLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHG .* ****.** *****.**. ****. **.******
336"	LEDKVELTPVAIQAGRLLAQRLYAGSTVKCDYENVPTTVFTPLEYGACGLSEEKAVEKFG
418′	QEHVEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPTAGAGPAFSLAPTQGEVTQGFAL .***** ***.******* * * * *
396"	EENIEVYHSYFWPLEWTIPSRDNNKCYAKIICNTKDNERVVG-FHVLGPNAGEVTQGFAA
478'	GIKCGASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCSeCysG***
155"	ALKCGLTKKQLDSTIGIHPVCAEVFTTLSVTKRSGASILQAGCSeCysG

Figure 2



FUZUEG SUZUES

Figure 3

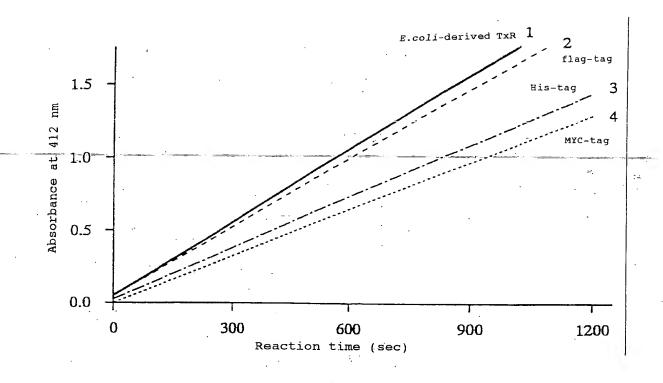


Figure 4

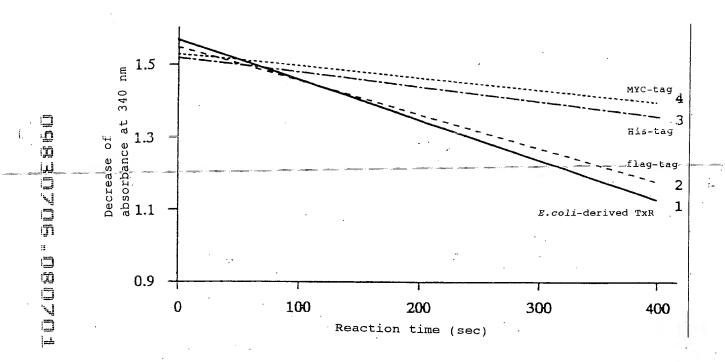
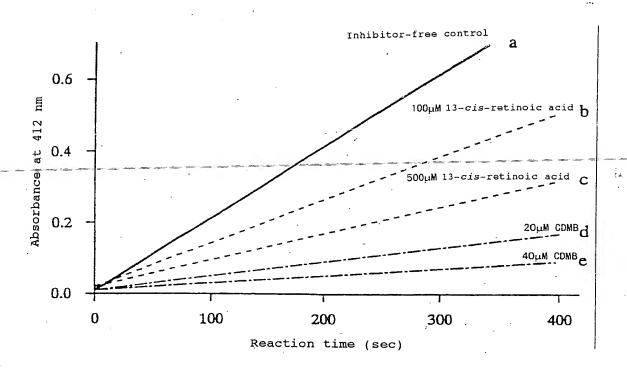


Figure 5



ngeinzoe - oeozot